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SEQUENCE LISTING

<11> Hauptmann, Rudolph  
Hummeler, Adolph  
Maurer-Pögy, Ingrid  
Sratowa, Christian

<12> TNF Receptors, TNF Binding Proteins and DNAs Coding for Them

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<141> 1,000-03-15

<15> 06,385,616  
<151> 1,000-02-01

<15> 07,153,247  
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<17> PatentIn Ver. 2.0

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<222> (606)..(633)  
<223> Portion of TNF-BP pro protein cleaved by extracellular proteases following secretion.

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 gag ctg ttg gtg gga ata tac ctc ggc gtc att gga ctg gtc ctc 98  
 Glu Leu Leu Val Gly Ile Tyr Pro Ser Gly Val Ile Gly Leu Val Pro  
 20 25 30  
 ctc ata ggg gac agg gag aag aat gat agt gtg tgc ctc caa tga aat 144  
 His Leu Gly Asp Arg Glu Lys Arg Asp Ser Val Cys Pro Gln Gly Lys  
 35 40 45  
 tat atc ctc ctc caa aat aat tgc att tgc tgc aac aac tgc ctc aat 192  
 Tyr Ile His Pro Gln Asn Asn Ser Ile Cys Cys Thr Lys Cys His Lys  
 50 55 60  
 gga acc tac ttg tac aat gac tgc ctc ggc ccc gug cag gat aac gac 240  
 Gly Thr Tyr Leu Tyr Asn Asp Cys Pro Gly Pro Gln Asp Thr Asp  
 65 70 75 80  
 tgc agg gag tgc gag aac ggc tcc ttc acc gtc tca gaa aac ctc ctc 288  
 Cys Arg Glu Cys Glu Ser Gly Ser Phe Thr Ala Ser Glu Asn His Leu  
 95 100 105 110  
 aac cac tgc ctc aac tgc tcc aac tgc ctc aac aag gaa atg ggt cag gtg 336  
 Arg His Cys Leu Ser Cys Ser Lys Cys Arg Lys Glu Met Gly Gln Val  
 100 105 110  
 gag atc tct tct tgc aca gtg gac cgg gac acc gtg tgc ggc tgc agg 384  
 Gln Ile Ser Ser Cys Thr Val Asp Arg Asp Thr Val Cys Gly Cys Arg  
 115 120 125  
 aac aac cag tac cgg cat tat tgc aat gaa aac ctt ttc cag tgc ttc 432  
 Lys Asn Gln Tyr Arg His Tyr Trp Ser Glu Asn Leu Phe Gln Cys Phe  
 130 135 140  
 aat tgc aac ctc tgc ctc aat ggg acc gtg ctc ctc tgc cag gag 480  
 Asn Cys Ser Leu Cys Leu Asn Gly Thr Val His Leu Ser Cys Gln Glu  
 145 150 155 160  
 aaa cag aac acc gtg tgc acc tgc cat gca gtc ttc ttt cta aca gaa 528  
 Lys Gln Asn Thr Val Cys Thr Cys His Ala Gly Phe Phe Leu Arg Glu  
 165 170 175  
 aac gag tgc tcc tgc tgc aat gac aac tgc gag aac tgc gag tgc aac 576  
 Asn Glu Cys Val Ser Cys Ser Asn Cys Lys Lys Ser Leu Glu Cys Thr  
 180 185 190  
 aag ttg tgc cta ccc cag att ggc aat gtt aac ggc act gag gag gac tca 624  
 Lys Leu Cys Leu Pro Gln Ile Gln Asn Val Lys Gly Thr Glu Asp Ser  
 195 200 205  
 ggc acc aca gtg ctc ttg ccc ctc gtc att ttc ttt ggt ctt tgc ctc 672  
 Gly Thr Thr Val Leu Leu Pro Leu Val Ile Phe Phe Gly Leu Cys Leu  
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Ser Lys Leu Tyr Ser Ile Val Cys Gly Lys Ser Thr Pro Glu Lys Glu			
245	250	255	
ggg gag ctt gaa gga act act act aag ccc ctg ggc cca aac cca aac			816
Gly Glu Leu Glu Gly Thr Thr Lys Pro Leu Ala Pro Asn Pro Ser			
260	265	270	
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Phe Ser Pro Thr Pro Gly Phe Thr Pro Thr Leu Gly Phe Ser Pro Val			
275	280	285	
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Pro Ser Ser Thr Phe Thr Ser Ser Thr Tyr Thr Pro Gly Asp Cys			
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ccc aac ttt gag gtc ccc aca gag gtc gca ccc ccc tat cag ggg			960
Pro Asn Phe Ala Ala Pro Arg Arg Glu Val Ala Pro Pro Tyr Gln Gly			
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gtc gag ccc atc ctt gca aca gca ctc gcc tcc gag ccc atc ccc aac			1008
Ala Asp Pro Ile Leu Ala Thr Ala Leu Ala Ser Asp Pro Ile Pro Asn			
325	330	335	
ccc ctt gag aag tgg gag gag aac gac aac aca cag aac cta gag			1056
Pro Leu Gln Lys Trp Glu Asp Ser Ala His Lys Pro Gln Ser Leu Asp			
340	345	350	
act gat gag ccc gcg aac ctg tac gac gtc gtg gag aac gtc ccc ccc			1104
Thr Asp Asp Pro Ala Thr Leu Tyr Ala Val Val Glu Asn Val Pro Pro			
355	360	365	
ttg cgc tgg aag gaa ttg gtg cgg cgc cta ggg ctg aac gag ccc gag			1152
Leu Arg Trp Lys Glu Phe Val Arg Arg Leu Gly Leu Ser Asp His Glu			
370	375	380	
atc gat cgg ctg gag ctg cag aac ggg cgc tgc ctg cgc gag ggg caa			1200
Ile Asp Arg Leu Glu Leu Gln Asn Gly Arg Cys Leu Arg Glu Ala Gln			
385	390	395	400
tac aac atg ctg gcg aac tgg aac cgg cgc aac ccc cgg cgc gag gcc			1248
Tyr Ser Met Leu Ala Thr Trp Arg Arg Arg Thr Pro Arg Arg Glu Ala			
405	410	415	
acc ctg gag ctg ctg gga cgc gtc ctc cgc gag atg gag ctg ctg ggc			1296
Tyr Leu Glu Leu Leu Gly Arg Val Leu Arg Asp Met Asp Leu Leu Gly			
420	425	430	
tgc ctg gag gag atc gag gag ggc ctt tgc ggc ccc gcc gcc ctc ccc			1344
Cys Leu Glu Asp Ile Glu Ala Leu Cys Gly Pro Ala Ala Leu Pro			
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ccc gcg ccc agt ctt ctc aga tga			1368
Pro Ala Pro Ser Leu Leu Arg			

450

455

210 - 2  
 211 - 455  
 212 - IRT  
 213 - Homo sapiens

210 - 2  
 211 - 455  
 212 - IRT  
 213 - Homo sapiens

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Glu Leu Leu Val Gly Ile Tyr Pro Ser Gly Val Ile Gly Leu Val Pro  
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His Leu Gly Asp Arg Glu Lys Arg Asp Ser Val Cys Pro Gln Gly Lys  
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Tyr Ile His Pro Gln Asn Asn Ser Ile Cys Cys Thr Lys Cys His Lys  
 50 55 60

Gly Thr Tyr Leu Tyr Asn Asp Cys Pro Gly Pro Gln Asp Thr Asp  
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Cys Arg Glu Cys Glu Ser Gly Ser Phe Thr Ala Ser Gln Asn His Leu  
 85 90 95

Arg His Cys Leu Ser Cys Ser Lys Cys Arg Lys Gln Met Gly Gln Val  
 100 105 110

Glu Ile Ser Ser Cys Thr Val Asp Arg Asp Thr Val Cys Gly Cys Arg  
 115 120 125

Lys Asn Gln Tyr Arg His Tyr Trp Ser Glu Asn Leu Phe Gln Cys Phe  
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 145 150 155 160

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 165 170 175

Asn Glu Cys Val Ser Cys Ser Asn Cys Lys Ser Leu Gln Cys Thr  
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Lys Leu Cys Leu Pro Gln Ile Gln Asn Val Lys Gly Thr Glu Asp Ser  
 195 200 205

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370 375 380

Ile Asp Arg Leu Glu Leu Gln Asn Gly Arg Cys Leu Arg Glu Ala Gln  
390 395 400

Tyr Ser Met Leu Ala Thr Trp Arg Arg Arg Thr Pro Arg Arg Glu Ala  
405 410 415

Thr Leu Glu Leu Leu Gly Arg Val Leu Arg Asp Met Asp Leu Leu Gly  
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Pro Ala Pro Ser Leu Leu Arg  
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<1>13..Homo sapiens

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Ile Cys Cys Thr Lys Cys His Lys Gly Thr Tyr Leu Tyr Asn Asp Cys  
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Pro	Gly	Pro	Gly	Gln	Asp	Thr	Asp	Cys	Arg	Glu	Cys	Glu	Ser	Gly	Ser	
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ttc	acc	gtc	tca	gaa	aac	aac	ctc	aga	acg	tgc	acc	tcc	aaa		192	
Phe	Thr	Ala	Ser	Glu	Asn	His	Leu	Arg	His	Cys	Leu	Ser	Cys	Ser	Lys	
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tgc	ccg	aaq	gaa	atg	gtg	cag	gtg	atc	tct	tct	tgc	acc	gtg	gac		240
Cys	Arg	Lys	Glu	Met	Gly	Gln	Val	Ser	Ile	Ser	Ser	Cys	Thr	Val	Asp	
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ccg	pac	acc	gtg	tat	ggc	tgc	agg	aac	ccg	tac	ccg	att	tat	tgg		288
Arg	Asp	Thr	Val	Cys	Gly	Cys	Arg	Asn	Gln	Tyr	Arg	His	Tyr	Trp		
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aat	aae	att	tcc	cag	tgc	tcc	aat	tgc	acg	ctc	tgc	ccg	aat	gag		336
Ser	Glu	Asn	Leu	Phe	Gln	Cys	Phe	Arg	Cys	Ser	Leu	Cys	Leu	Asn	Gly	
100																100
acc	atc	pac	ctc	tcc	tgc	cag	gag	aaa	cag	aac	acc	gtg	tgc	acc	tcc	384
Thr	Val	His	Leu	Ser	Cys	Gln	Glu	Lys	Gln	Asn	Thr	Val	Cys	Thr	Cys	
115																115
aat	aca	gtt	tcc	ttt	cta	aga	gaa	aac	gag	tgt	gtc	tcc	tgt	agt	aac	432
His	Ala	Gly	Phe	Phe	Leu	Arg	Glu	Asn	Glu	Cys	Val	Ser	Cys	Ser	Asn	
130																130
aat	aaa	acg	ctg	gag	tgc	acg	aaq	ttg	tgc	cta	ccc	cag	att	gag		480
Cys	Lys	Ser	Leu	Glu	Cys	Thr	Lys	Leu	Cys	Leu	Pro	Gln	Ile	Glu		
145																145
aat																483
Asn																

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<113 - Homo sapiens

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20																30
Pro	Gly	Pro	Gly	Gln	Asp	Thr	Asp	Cys	Arg	Glu	Cys	Glu	Ser	Gly	Ser	
35																45
Phe	Thr	Ala	Ser	Glu	Asn	His	Leu	Arg	His	Cys	Leu	Ser	Cys	Ser	Lys	
50																50
Cys	Arg	Lys	Glu	Met	Gly	Gln	Val	Glu	Ile	Ser	Ser	Cys	Thr	Val	Asp	
65																65
70																70
75																75
80																80

Arg Asp Thr Val Cys Gly Cys Arg Lys Asn Gln Tyr Arg His Tyr Trp  
85 90 95

Ser Gln Asn Leu Thr Gln Cys Phe Asn Cys Ser Leu Cys Leu Asn Gly  
100 105 110

Thr Val His Leu Ser Cys Gln Glu Lys Gln Asn Thr Val Cys Thr Cys  
115 120 125

His Ala Gly Phe Phe Leu Arg Glu Asn Glu Cys Val Ser Cys Ser Asn  
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gag ctg ttg gtt gga ata tac ccc tca ggg gtt att gga 87  
Glu Leu Leu Val Gly Ile Tyr Pro Ser Gly Val Ile Gly  
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Glu Asn Val Lys Gly Thr Glu Asp Ser Gly Thr Thr Val Ile Leu Pro			
100	205	210	215
ttt gtt att ttc ttg ggt ctt tgc ctt ttatcc ctc ctc ttc att ggt			905
Leu Val Ile Phe Phe Gly Leu Cys Leu Leu Ser Leu Leu Phe Ile Gly			
220	225	230	
ttt atq tat ctc tac caa cgg tgg aag tcc aag ctc tac tcc att gtt			953
Leu Met Tyr Arg Tyr Glu Gln Arg Trp Lys Ser Lys Leu Tyr Ser Ile Val			
235	240	245	
tgt tgg daa ttp tca cct gaa aac gat ggg gaa ctt gaa ggt att aat			1001
Cys Gly Lys Ser Thr Pro Glu Lys Glu Gly Glu Leu Glu Gly Thr Thr			
250	255	260	
atc tgg ccc ctc gtc cca aat cca aag ttc aat ccc act cca ggc ttc			1049
Thr Lys Pro Leu Ala Pro Asn Pro Ser Phe Ser Pro Thr Pro Gly Phe			
265	270	275	
acc ccc acc ctc ggc ttc aat ccc gtc aat tcc acc ttc acc tcc			1057
Thr Pro Thr Leu Gly Phe Ser Pro Val Pro Ser Ser Thr Phe Thr Ser			
280	285	290	295
aga tcc acc tat acc ccc ggt gac tgg ccc aat ttt gct ccc cgc			1145
Ser Ser Thr Tyr Thr Pro Gly Asp Cys Pro Asn Phe Ala Ala Pro Arg			
300	305	310	
aga gag gtg gca cca ccc tat caa gga gct gac ccc atc ctt gct aca			1193
Arg Glu Val Ala Pro Pro Tyr Glu Gly Ala Asp Pro Ile Leu Ala Thr			
315	320	325	
gcc ctc gcc tcc gac ccc atc ccc aac ccc ctt cag aag tgg gag gac			1241
Ala Leu Ala Ser Asp Pro Ile Phe Asn Pro Leu Glu Lys Trp Glu Asp			
330	335	340	
agc gcc cac aag cca cag agc cta gac act gat gac ccc gct acg ctg			1289
Ser Ala His Lys Pro Gln Ser Leu Asp Thr Asp Asp Pro Ala Thr Leu			
345	350	355	
tac ccc gtg gng gag aac gtg ccc ccc ttg cgc tgg aaggaattc			1334
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 lambdaTNF-BP15 and pTNF-BP15 vectors

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Glu Leu Leu Val Gly Ile Tyr Pro Ser Gly Val Ile Gly Leu Val Pro  
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His Leu Gly Asp Arg Glu Lys Arg Asp Ser Val Cys Pro Glu Gly Lys  
15 30 45

Tyr Ile His Pro Gln Asn Asn Ser Ile Cys Cys Thr Lys Cys His Lys  
50 55 60

Gly Thr Tyr Leu Tyr Asn Asp Cys Pro Gly Pro Gln Asp Thr Asp  
65 70 75 80

Cys Arg Glu Cys Glu Ser Gly Ser Phe Thr Ala Ser Glu Asn His Leu  
85 90 95

Arg His Cys Leu Ser Cys Ser Lys Cys Arg Lys Glu Met Gly Gln Val  
100 105 110

Glu Ile Ser Ser Cys Thr Val A.p Arg Asp Thr Val Cys Gly Cys Arg  
115 120 125

Lys Asn Gln Tyr Arg His Tyr Tip Ser Glu Asn Leu Phe Gln Cys Phe  
130 135 140

Asn Cys Ser Leu Cys Leu Asn Gly Thr Val His Leu Ser Cys Gln Glu  
145 150 155 160

Lys Gln Asn Thr Val Cys Thr Cys His Ala Gly Phe Phe Leu Arg Glu  
165 170 175

Asn Glu Cys Val Ser Cys Ser Asn Cys Lys Lys Ser Leu Glu Cys Thr  
180 185 190

Lys Leu Cys Leu Pro Gln Ile Glu Asn Val Lys Glu Tar Glu Asp Ser  
195 200 205

Gly Thr Thr Val Leu Leu Pro Leu Val Ile Phe Phe Gly Leu Cys Leu  
210 215 220

Leu Ser Leu Leu Phe Ile Gly Leu Met Tyr Arg Tyr Gln Arg Trp Lys  
225 230 235 240

Ser Lys Leu Tyr Ser Ile Val Cys Gly Lys Ser Thr Pro Glu Lys Glu  
245 250 255

Gly Glu Leu Glu Gly Thr Thr Lys Pro Leu Ala Pro Asn Pro Ser  
260 265 270

Phe Ser Pro Thr Pro Gly Phe Thr Pro Thr Leu Gly Phe Ser Pro Val  
275 280 285

Pro Ser Ser Thr Phe Thr Ser Ser Thr Tyr Thr Pro Gly Asp Cys  
290 295 300

Pro Asn Phe Ala Ala Pro Arg Arg Glu Val Ala Pro Pro Tyr Gln Gly  
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Ala Asp Pro Ile Leu Ala Thr Ala Leu Ala Ser Asp Ile Ile Pro Asn  
325 330 335

Pro Leu Gln Lys Trp Glu Asp Ser Ala His Lys Pro Gln Ser Leu Asp  
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Thr Asp Asp Pro Ala Thr Leu Tyr Ala Val Val Glu Asn Val Pro Pro  
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Leu Arg Trp  
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3210- 13

3211- 6414

3212- DNA

3213- Artificial Sequence

32140-

32141- Description of Artificial Sequence: pADCMV1 vector

32142-

32143- unsure

32144- (344)

32145- "n" can be a, g, c, or t

32146-

32147- unsure

32148- (4157)

32149- "n" can be a, g, c, or t

32150-

32151- unsure

32152- (5135)

32153- "n" can be a, g, c, or t

32154-

32155- unsure

32156- (6255)

32157- "n" can be a, g, c, or t

32158- 13

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ccacgacccc cggccatttga cgtcaataat gacgtatgtt cccatagtaa cgcataatagg 180

gactttccat tgacgtcaat qqgtggagta tttacggtaa actgcggact tggcaagtaca 240

tcaatgttat catatccaa gtacgcccc tattgacgtc aatgacggtt aatggccgc 300

ctggcattat gcccagtaca tgacattatg ggactttctt actnggcagt acatctaagt 360





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gaaaacccatc ttacggatccatc tccatccatc tccatccatc tccatccatc tccatccatc tccatccatc 5160  
agtgataaca ctggggccaa tccatccatc tccatccatc tccatccatc tccatccatc tccatccatc 5220  
gttttttgc acaacatccatc tccatccatc tccatccatc tccatccatc tccatccatc tccatccatc 5280  
aatgaaatccatc tccatccatc tccatccatc tccatccatc tccatccatc tccatccatc tccatccatc 5340  
ttgcgcggaaat tattaaatccatc tccatccatc tccatccatc tccatccatc tccatccatc tccatccatc 5400  
tggatggaggccatccatc cccatccatc tccatccatc tccatccatc tccatccatc tccatccatc tccatccatc 5460

<..10> 14  
<..11> 2173  
<..12> DNA  
<..13> Artificial Sequence

<11.0>  
<11.1> CDS  
<11.2> (245) .. (1630)

9123. Description of Artificial Sequence: ratTNF-R8

<4:0> 14  
 gaattccctt ttcggaggt ttctgaactc tggctcatga tggggcttac tggataacgg 60  
 aatccctggag gaccgtaccc tgatttccat ctacctctga ctttggaecc ttctaaaccc 120  
 gggctcaagc tgccaaacacc cggggccaccc ggtccgatcg tcttaactca ttcaccaggc 180  
 ttgtccaaattg ctgtccctgtc ccggcccca atgggggaggt gagagaggcc aatgtccggcc 240  
 ggac atg ggt ctc ccc atc gtg cct ggc ctg ctg tca ctg gtg ctc 289  
     Met Gly Leu Pro Ile Val Pro Gly Leu Leu Leu Ser Leu Val Leu  
     1           5           10           15

5

10

15



agg	ccc	agg	gtc	taa	atc	att	tgt	agg	gat	tca	gtt	ctt	gtc	aaa	1009		
Arg		Pro	Arg	Val	Tyr	Ser	Ile	Ile	Cys	Arg	Asp	Ser	Ala	Pro	Val	Lys	
240															245	250	255
ttt	ttt																
Leu	Val	Glu	Gly	Glu	Gly	Gly	Ile	Val	Thr	Lys	Pro	Leu	Thr	Pro	Ala	Ser	
															260	265	270
ttt	ttt																
Leu	Val	Glu	Gly	Glu	Gly	Gly	Ile	Val	Thr	Lys	Pro	Leu	Thr	Pro	Ala	Ser	
															275	280	285
ttt	ttt																
Leu	Pro	Ala	Phe	Ser	Pro	Asn	Pro	Gly	Phe	Asn	Pro	Thr	Leu	Gly	Phe		
															290	295	300
ttt	ttt																
Leu	Pro	Arg	Phe	Ser	Pro	Val	Ser	Thr	Pro	Leu	Ser	Thr	Pro	Ile	Ser		
															305	310	315
ttt	ttt																
Leu	Pro	Val	Phe	Gly	Pro	Ser	Asn	Trp	His	Asn	Phe	Val	Pro	Pro	Val	Arg	
															320	325	330
ttt	ttt																
Leu	Val	Val	Pro	Thr	Gln	Gly	Ala	Asp	Pro	Leu	Leu	Tyr	Gly	Ser	Leu		
															335	340	345
ttt	ttt																
Leu	Pro	Val	Pro	Ile	Pro	Ala	Pro	Val	Arg	Lys	Trp	Glu	Asp	Val	Val		
															350	355	360
ttt	ttt																
Leu	Ala	Gln	Pro	Gln	Arg	Leu	Asp	Thr	Ala	Asp	Pro	Ala	Met	Leu	Tyr		
															365	370	375
ttt	ttt																
Leu	Val	Val	Asp	Gly	Val	Pro	Pro	Thr	Arg	Trp	Lys	Glu	Phe	Met	Arg		
															380	385	390
ttt	ttt																
Leu	Leu	Gly	Leu	Ser	Gl	His	Glu	Ile	Glu	Arg	Leu	Gl	Leu	Gln	Asn		
															395	400	405
ttt	ttt																
Leu	Leu	Gly	Leu	Arg	Gly	Ala	Tyr	Ser	Met	Leu	Glu	Ala	Trp	Arg			
															410	415	420
ttt	ttt																
Leu	Arg	Arg	Thr	Pro	Arg	His	Glu	Ala	Thr	Leu	Asp	Val	Val	Gly	Arg	Val	
															425	430	435
ttt	ttt																
Leu	Cys	Asp	Met	Asn	Leu	Arg	Gly	Cys	Leu	Glu	Asn	Ile	Arg	Glu	Thr		
															440	445	450
ttt	ttt																
Leu	Glu	Ser	Pro	Ala	His	Ser	Ser	Thr	Thr	His	Leu	Pro	Arg				
															455	460	465
ttt	ttt																
Leu	Glu	Ser	Pro	Ala	His	Ser	Ser	Thr	Thr	His	Leu	Pro	Arg				
															470	475	480
ttt	ttt																
Leu	Glu	Ser	Pro	Ala	His	Ser	Ser	Thr	Thr	His	Leu	Pro	Arg				
															485	490	495
ttt	ttt																
Leu	Glu	Ser	Pro	Ala	His	Ser	Ser	Thr	Thr	His	Leu	Pro	Arg				
															500	505	510
ttt	ttt																
Leu	Glu	Ser	Pro	Ala	His	Ser	Ser	Thr	Thr	His	Leu	Pro	Arg				
															515	520	525
ttt	ttt																
Leu	Glu	Ser	Pro	Ala	His	Ser	Ser	Thr	Thr	His	Leu	Pro	Arg				
															530	535	540
ttt	ttt																
Leu	Glu	Ser	Pro	Ala	His	Ser	Ser	Thr	Thr	His	Leu	Pro	Arg				
															545	550	555
ttt	ttt																
Leu	Glu	Ser	Pro	Ala	His	Ser	Ser	Thr	Thr	His	Leu	Pro	Arg				
															560	565	570
ttt	ttt																
Leu	Glu	Ser	Pro	Ala	His	Ser	Ser	Thr	Thr	His	Leu	Pro	Arg				
															575	580	585
ttt	ttt																
Leu	Glu	Ser	Pro	Ala	His	Ser	Ser	Thr	Thr	His	Leu	Pro	Arg				
															590	595	600

ccctgtgaacc tcctctttgg tcctcttagg ggcacqcteg atctggcagg ctccatctgg 1750  
cagccacttc ctttgtqeta cccacttggt gtatataqet ttcccaqgtt qccqaggaca 1810  
gcctgtgcca qccacttqtg catggcaggg aagtgtgcca tctgttccaa qaaqatgtgag 1870  
qgtgccaada qccaggqagag gtgttttgtg aaaaaaaca caatctatc qataccact 1930  
tggatgcaa qqaaccaaaac aaqatcttc aggctctt cagtqatit ctggccctt 1990  
ttcacagtat ataaaaactt ctttgttattt attatataac actaatqptt qccacttqa 2050  
actccctaag qtagggcaca qcacaguaca gtggggcttc cagctq;agc cccgactct 2110  
tqtaataaca cttaadatct aaaaqtqada aaaaadada aaaaadada aaaaaaggaa 2170  
ttc 2173

<#10> 15

<#11> 461

<#12> PRT

<#13> Artificial Sequence

<#10>

<#13> Description of Artificial Sequence: ratTNF-R3

<#10> 15

Met Gly Leu Pro Ile Val Pro Gly Leu Leu Ser Leu Val Leu Leu  
1 5 10 15

Ala Leu Leu Met Gly Ile His Pro Ser Gly Val Thr Gly Leu Val Pro  
20 25 30

Ser Leu Gly Asp Arg Glu Lys Arg Asp Asn Leu Cys Pro Gln Gly Lys  
35 40 45

Tyr Ala His Pro Lys Asn Asn Ser Ile Cys Cys Thr Lys Cys His Lys  
50 55 60

Gly Thr Tyr Leu Val Ser Asp Cys Pro Ser Pro Gly Gln Glu Thr Val  
65 70 75 80

Cys Glu Leu Ser His Lys Gly Thr Phe Thr Ala Ser Gln Asn His Val  
85 90 95

Arg Gln Cys Leu Ser Cys Lys Thr Cys Arg Lys Glu Met Phe Gln Val  
100 105 110

Gln Ile Ser Pro Cys Lys Ala Asp Met Asp Thr Val Cys Gly Cys Lys  
115 120 125

Lys Asn Gln Phe Gln Arg Tyr Leu Ser Glu Thr His Phe Gln Cys Val  
130 135 140

Asp Cys Ser Pro Cys Phe Asn Gly Thr Val Thr Ile Pro Cys Lys Glu

145	150	155	160
Lys Gln Asn Thr Val Cys Asn Cys His Ala Gly Phe Phe Leu Ser Gly			
165	170	175	
Asn Glu Cys Thr Pro Cys Ser His Cys Lys Lys Asn Gln Glu Cys Met			
180	185	190	
Lys Leu Cys Leu Pro Pro Val Ala Asn Val Thr Asn Pro Gln Asp Ser			
195	200	205	
Gly Thr Ala Val Ser Leu Pro Leu Val Ile Phe Leu Gly Leu Cys Leu			
210	215	220	
Leu Phe Ile Ile Cys Ile Ser Leu Leu Cys Arg Tyr Pro Gln Trp Arg			
225	230	235	240
Pro Arg Val Tyr Ser Ile Ile Cys Arg Asp Ser Ala Pro Val Lys Glu			
245	250	255	
Val Glu Gly Glu Gly Ile Val Thr Lys Pro Leu Thr Pro Ala Ser Ile			
260	265	270	
Pro Ala Phe Ser Pro Asn Pro Gly Phe Asn Pro Thr Leu Gly Phe Ser			
275	280	285	
Thr Thr Pro Arg Phe Ser His Pro Val Ser Ser Thr Pro Ile Ser Pro			
290	295	300	
Val Phe Gly Pro Ser Asn Trp His Asn Phe Val Pro Pro Val Arg Glu			
305	310	315	320
Val Val Pro Thr Gln Gly Ala Asp Pro Leu Leu Tyr Gly Ser Leu Asn			
325	330	335	
Pro Val Pro Ile Pro Ala Pro Val Arg Lys Trp Glu Asp Val Val Ala			
340	345	350	
Ala Gln Pro Gln Arg Leu Asp Thr Ala Asp Pro Ala Met Leu Tyr Ala			
355	360	365	
Val Val Asp Gly Val Pro Pro Thr Arg Trp Lys Glu Phe Met Arg Leu			
370	375	380	
Leu Gly Leu Ser Glu His Glu Ile Glu Arg Leu Glu Leu Gln Asn Gly			
385	390	395	400
Arg Cys Leu Arg Glu Ala His Tyr Ser Met Leu Glu Ala Trp Arg Arg			
405	410	415	
Arg Thr Pro Arg His Gln Ala Thr Leu Asp Val Val Gly Arg Val Leu			
420	425	430	
Cys Asp Met Asn Leu Arg Gly Cys Leu Glu Asn Ile Arg Glu Thr Leu			
435	440	445	
Glu Ser Pro Ala His Ser Ser Thr Thr His Leu Pro Arg			

450

455

460

• z10 • 16  
 • z11 • z141  
 • z12 • DNA  
 • z13 • Artificial Sequence

• z10 •  
 • z21 • CDS  
 • z22 • (z13) .. (1580)

• z20 •  
 • z23 • Description of Artificial Sequence: human TNF-**R**1  
 TNF-**R**2

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 cttgtatctc tatccccgag tctcaacccct caactgtcac cccaaaggcac ttggggacgac 120  
 ctggacaaqac cgagtcggcg gaagccccag cactgcccgtt gccacactgc ctttqagccca 180  
 kicqyqqqag tgagaggeca tagstgtctg gc atg ggc ttc tcc acc qtg cct 232  
 Met Gly Leu Ser Thr Val Pro  
 1 5  
 gac ctg ctg ctg cca ctg gtc ctg gag ctg ttg gtg gga ata tac 281  
 Asp Leu Leu Leu Pro Leu Val Leu Leu Glu Leu Leu Val Gly Ile Tyr  
 10 15 20  
 ccc tca ggg gtt att gga ctg gtc cct cac cta qgg gac agg gag aag 329  
 Pro Ser Gly Val Ile Gly Leu Val Pro His Leu Gly Asp Arg Glu Lys  
 25 30 35  
 aga gat aqt gtg tgt ccc caa gga aaa tat atc cac cct caa aat aat 377  
 Arg Asp Ser Val Cys Pro Gln Gly Lys Tyr Ile His Pro Gln Asn Asn  
 40 45 50 55  
 tcc att tgc tgc acc aag tgc cac aaa gga acc tac ttg tcc aat gac 425  
 Ser Ile Cys Cys Thr Lys Cys His Lys Gly Thr Tyr Leu Tyr Asn Asp  
 60 65 70  
 tgc cca ggc ccc ggg cag gat aqc gac tgc agg gag tgc gag aqc ggc 473  
 Cys Pro Gly Pro Gly Gln Asp Thr Asp Cys Arg Glu Cys Glu Ser Gly  
 75 80 85  
 tcc ttc acc qct tca gaa aac cac ctc aga cac tgc ctc aqc tgc tcc 521  
 Ser Phe Thr Ala Ser Glu Asn His Leu Arg His Cys Leu Ser Cys Ser  
 90 95 100  
 aaa tgc cga aag gaa atg ggt cag gtg gag atc tct tct tgc aca gtg 569  
 Lys Cys Arg Lys Glu Met Gly Gln Val Glu Ile Ser Ser Cys Thr Val  
 105 110 115  
 gac cgg gac acc qtg tgc ggc tgc agg aag aac cag tac cgg cat tat 617  
 Asp Arg Asp Thr Val Cys Gly Cys Arg Lys Asn Gln Tyr Arg His Tyr

120	125	130	135	
tgg aqt gaa aac ctt ttc cag tgc ttc aat tgc aqc ctc tgc ctc aat				661
Trp Ser Glu Asn Leu Phe Gln Cys Phe Asn Cys Ser Leu Cys Leu Asn				
149	144	149	154	
ggg aac gtc aac ctc tcc tgc cag gag aac ccc aac aat atp tgc aat				715
Gly Thr Val His Leu Ser Cys Gln Glu Lys Gln Asn Thr Val Cys Thr				
159	160	165	166	
tgc aat gca ggt ttc ttt cta aca gaa aac gag tgc gtc tcc tgc aat				761
Cys His Ala Gly Phe Phe Leu Arg Glu Asn Glu Cys Val Ser Cys Ser				
170	175	179	180	
aaa tgc aac aca aac ctc gag tgc aac aag ttc tgc cta ccc aac att				809
Asn Cys Lys Lys Ser Leu Glu Cys Thr Lys Leu Cys Leu Pro Gln Ile				
185	190	195	196	
atg aat gtt aac aac act gag gac tca gg. acc aca gtc ctc tgc aac				857
Gln Asn Val Lys Gly Thr Glu Asp Ser Gly Thr Thr Val Leu Leu Ile				
196	201	210	215	
ctc gtc att ttc ttt ggt ctt tgc ctt tta tcc ctc ctc ttc att ggt				905
Leu Val Ile Phe Phe Gly Leu Cys Leu Leu Ser Leu Leu Ile Gly				
220	225	230	235	
tta atg tat ctc tac caa cgg tgg aag tcc aac ctc tac tcc att gtt				953
Leu Met Tyr Arg Tyr Gln Arg Trp Lys Ser Lys Leu Tyr Ser Ile Val				
235	240	245	250	
tgt ggg aaa tcc aca ccc gaa aac gag ggg gag ctt gaa gga act act				1001
Cys Gly Lys Ser Thr Pro Glu Lys Gln Glu Leu Glu Gly Thr Thr				
250	255	260	265	
act aac ccc ctc ggc cca aac cca aac ttc agt ccc act cca ggc ttc				1049
Thr Lys Pro Leu Ala Pro Asn Pro Ser Phe Ser Pro Thr Pro Gly Phe				
265	270	275	280	
acc ccc acc ctc ggc ttc agt ccc gtg ccc agt tcc acc ttc acc tcc				1097
Thr Pro Thr Leu Gly Phe Ser Pro Val Pro Ser Ser Thr Phe Thr Ser				
280	285	290	295	
aga tcc acc tat acc ccc ggt gac tgc ccc aac ttt gcc gtc ccc ccc				1145
Ser Ser Thr Tyr Thr Pro Gly Asp Cys Pro Asn Phe Ala Ala Pro Arg				
300	305	310	315	
aga gag gtg gca cca ccc tat ccc ggg gtc gac ccc aac ctt gcc aca				1193
Arg Glu Val Ala Pro Pro Tyr Gln Gly Ala Asp Pro Ile Leu Ala Thr				
315	320	325	330	
gcc ctc gcc tcc gag acc atc ccc aac ccc ctt ccc aac tgg gag gag				1241
Ala Leu Ala Ser Asp Pro Ile Pro Asn Pro Leu Gln Lys Trp Glu Asp				
330	335	340	345	
agc gca cac aac ccc ccc aac				1289
Ser Ala His Lys Pro Gln Ser Leu Asp Thr Asp Asp Pro Ala Thr Leu				
345	350	355	360	

tac gac gtg gtg gag aac gtg ccc ccg ttg cgc tgg aat gaa tt; gtg 1357  
 Tyr Ala Val Val Glu Asn Val Pro Pro Leu Arg Trp Lys Glu Phe Val  
 360 365 370 375  
 cgg cgc ata ggg ctg agc gac gag atc gat cgg ctc gag ctg cag 1385  
 Arg Arg Leu Gly Leu Ser Asp His Glu Ile Asp Arg Leu Glu Leu Gln  
 380 385 390  
 aac ggg cgc tgc ctg cgc gag ggg cta tac aac atc ctc ggg aac tgg 1413  
 Asn Gly Arg Cys Leu Arg Glu Ala Gln Tyr Ser Met Leu Ala Thr Trp  
 395 400 405  
 agg cgg cgc aac ccc cgg cgg gag ggc aac ctg gag ctg gga cgc 1441  
 Arg Arg Arg Thr Pro Arg Arg Glu Ala Thr Leu Glu Leu Leu Gly Arg  
 410 415 420  
 gtg ctc cgc gac atg gag ctg ctc ggc tgc ctg gag gac atc gag gag 1469  
 Val Leu Arg Asp Met Asp Leu Leu Gly Cys Leu Glu Asp Ile Glu Glu  
 425 430 435  
 gcg ctt tgc ggc ccc gcc gcc ctc ccc ccc ggg ccc agt ctt ctc aga 1527  
 Ala Leu Cys Gly Pro Ala Ala Leu Pro Pro Ala Pro Ser Leu Leu Arg  
 440 445 450 455  
 tga ggctgcggcc ctggggcag ctctaaggac cgtctgcga gatcgcccttc 1630  
  
 caacccact tttttctgga aaggaggggt ctgcagggg caagcaggag ctagcagecg 1690  
 cctacttgtt gctaaccct cgtatgtacat agtcttttctc agtgcgtgc ggcggccga 1750  
 cagtcaagcgc tggcggccgc gagagaggtg cgcggggc tcaagacgt gagttgggg 1810  
 ttttcggagga tgagggacgc tatgcctcat gcccgttttgc ggtgtctca ccagcaaggc 1870  
 tgcgtgggggg cccctgggtc gtccctgagc ctttttcaca gtgcataaggc agttttttt 1930  
 gtttttgttt tgttttgttt tgtttttaaa tcaatcatgt tacactaata gaaacttggc 1990  
 actctctgtgc cctctgcgtg gacaaggcaca tagcaagctg aactgtctca aggcaggggc 2050  
 gagcacggaa caatggggcc ttcajctgga gctgtggact ttgtacata cactaaaatt 2110  
 ctgaagttaa aaaaaaaaaa aaaaggaatt c 2141

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 <211> 455  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: human TNF-R in  
 1TNF-R2

<400> 17

Met Gly Leu Ser Thr Val Pro Asp Leu Leu Leu Pro Leu Val Leu Leu  
 1 5 10 14

Glu Leu Leu Val Gly Ile Tyr Pro Ser Gly Val Ile Gly Leu Val Pro  
 19 21 23

His Leu Gly Asp Arg Glu Lys Arg Asp Ser Val Cys Pro Gln Gly Lys  
 35 40 45

Tyr Ile His Pro Gln Asn Asn Ser Ile Cys Cys Thr Lys Cys His Lys  
 50 55 60

Gly Thr Tyr Leu Tyr Asn Asp Cys Pro Gly Pro Gln Asp Thr Asp  
 65 70 75 80

Cys Arg Glu Cys Glu Ser Gly Ser Phe Thr Ala Ser Glu Asn His Leu  
 85 90 95

Arg His Cys Leu Ser Cys Ser Lys Cys Arg Lys Glu Met Gly Gln Val  
 100 105 110

Glu Ile Ser Ser Cys Thr Val Asp Arg Asp Thr Val Cys Gly Cys Arg  
 115 120 125

Lys Asn Gln Tyr Arg His Tyr Trp Ser Glu Asn Leu Phe Gln Cys Phe  
 130 135 140

Asn Cys Ser Leu Cys Leu Asn Gly Thr Val His Leu Ser Cys Gln Glu  
 145 150 155 160

Lys Gln Asn Thr Val Cys Thr Cys His Ala Gly Phe Phe Leu Arg Glu  
 165 170 175

Asn Glu Cys Val Ser Cys Ser Asn Cys Lys Lys Ser Leu Glu Cys Thr  
 180 185 190

Lys Leu Cys Leu Pro Gln Ile Glu Asn Val Lys Gly Thr Glu Asp Ser  
 195 200 205

Gly Thr Thr Val Leu Leu Pro Leu Val Ile Phe Phe Gly Leu Cys Leu  
 210 215 220

Leu Ser Leu Leu Phe Ile Gly Leu Met Tyr Arg Tyr Gln Arg Trp Lys  
 225 230 235 240

Ser Lys Leu Tyr Ser Ile Val Cys Gly Lys Ser Thr Pro Glu Lys Glu  
 245 250 255

Gly Glu Leu Glu Gly Thr Thr Lys Pro Leu Ala Pro Asn Pro Ser  
 260 265 270

Phe Ser Pro Thr Pro Gly Phe Thr Pro Thr Leu Gly Phe Ser Pro Val  
 275 280 285

Pro Ser Ser Thr Phe Thr Ser Ser Ser Thr Tyr Thr Pro Gly Asp Cys  
 290 295 300

Pro Asn Phe Ala Ala Pro Arg Arg Glu Val Ala Pro Pro Tyr Gln Gly  
305 310 315 320

Ala Asp Pro Ile Leu Ala Thr Ala Leu Ala Ser Asp Pro Ile Pro Asn  
325 330 335

Ile Leu Gln Lys Trp Glu Asp Ser Ala His Lys Pro Gln Ile Leu Asp  
340 345 350

Thr Asp Asp Pro Ala Thr Leu Tyr Ala Val Val Glu Asn Val Pro Pro  
355 360 365

Leu Arg Trp Lys Glu Phe Val Arg Arg Leu Gly Leu Ser Asp His Glu  
370 375 380

Ile Asp Arg Leu Glu Leu Gln Asn Gly Arg Cys Leu Arg Glu Ala Gln  
385 390 395 400

Tyr Ser Met Leu Ala Thr Trp Arg Arg Arg Thr Pro Arg Arg Glu Ala  
405 410 415

Thr Leu Glu Leu Leu Gly Arg Val Leu Arg Asp Met Asp Leu Leu Gly  
420 425 430

Cys Leu Glu Asp Ile Glu Glu Ala Leu Cys Gly Pro Ala Ala Leu Pro  
435 440 445

Pro Ala Pro Ser Leu Leu Arg  
450 455

<0110> 18

<0111> 18

<0112> PRT

<0113> Artificial Sequence

<0120>

<0121> Description of Artificial Sequence: N-terminal  
amino acid sequence of protein purified from urine  
(main sequence)

<0122>

<0121> UNSURE

<0122> (4)

<0123> Identity of "Xaa" could not be determined.

<0100> 18

Asp Ser Val Xaa Pro Gln Gly Lys Tyr Ile His Pro Gln  
1 5 10

<0101> 19

<0111> 9

<0112> PRT

<0113> Artificial Sequence

<0220>

<200> Description of Artificial Sequence: N-terminal  
amino acid sequence of protein purified from urine  
(subsidiary sequence)

<210>

<211> UNSURE

<212> (1)

<213> Identity of "Xaa" could not be determined.

<400> 18

Leu Val Pro His Leu Gly Xaa Arg Glu

<210> 19

<211> 151

<212> rRNA

<213> Homo sapiens

<400> 20

caatccggaaa tatttacccct caaataatcc gatttgcgtgt accaagtgcg acaaaggaaa 60

tttttttttttatac aatgacttcc cagggccggg gcaggatacg qactgcgggg aatgtgtggag 120

ccgttttttttcc acagcccttag aaaacaacaa g

151

<210> 21

<211> 6

<212> PRT

<213> Artificial Sequence

<400>

<210> Description of Artificial Sequence: TNF-BP tryptic  
cleavage peptide

<210> 21

Asp Ser Val Cys Pro Gln Gly Lys

1 5

<210> 22

<211> 7

<212> PRT

<213> Artificial Sequence

<400>

<210> Description of Artificial Sequence: TNF-BP tryptic  
cleavage peptide

<210>

<211> UNSURE

<212> (1)...(2)

<213> Identity of "Xaa" could not be determined.

<400> 22

Xaa Xaa Leu Ser Cys Ser Lys

1

5

<210> 23

<211> 7

<212> PPT

<213> Artificial Sequence

<220>

<221> Description of Artificial Sequence: TNF-BP trypic cleavage peptide

<400> 23

A p Thr Val Cys Gly Cys Arg  
1 5

<100> 24

<110> 11

<111> PPT

<113> Artificial Sequence

<200>

<221> Description of Artificial Sequence: TNF-BP trypic cleavage peptide

<400> 24

Glu Asn Glu Cys Val Ser Cys Ser Asn Cys Lys  
1 5 10

<210> 25

<211> 12

<212> PPT

<213> Artificial Sequence

<200>

<221> Description of Artificial Sequence: TNF-BP trypic cleavage peptide

<400> 25

Glu Asn Glu Cys Val Ser Cys Ser Asn Cys Lys Lys  
1 5 10

<100> 26

<110> 13

<111> PPT

<113> Artificial Sequence

<200>

<221> Description of Artificial Sequence: TNF-BP trypic cleavage peptide

<210>

<211> UNSURE

<222> (6)

<223> Identity of "Xaa" could not be determined.

<210>

<211> UNMURE

<212> PRT

<223> Identity of "Xaa" could not be determined.

<400> 26

Tyr Ile His Pro Gln Xaa Asn Ser Ile Xaa Xaa Xaa Lys  
1 5 10

<210> 27

<211> 14

<212> PRT

<213> Artificial Sequence

<210>

<213> Description of Artificial Sequence: TNF-BP tryptic cleavage peptide

<400> 27

Glu Cys Glu Ser Gly Ser Phe Thr Ala Ser Glu Asn Asn Lys  
1 5 10

<210> 28

<211> 3

<212> PRT

<213> Artificial Sequence

<210>

<213> Description of Artificial Sequence: TNF-BP tryptic cleavage peptide

<400> 28

Leu Val Pro His Leu Gly Asp Arg  
1 5

<210> 29

<211> 15

<212> PRT

<213> Artificial Sequence

<210>

<213> Description of Artificial Sequence: TNF-BP tryptic cleavage peptide

<400> 29

Lys Glu Met Gly Gln Val Glu Ile Ser Ser Cys Thr Val Asp Arg  
1 5 10 15

<210> 30

<211> 15

<212> PRT

<213> Artificial Sequence

<200>

<220> Description of Artificial Sequence: TNF-BP tryptic cleavage peptide

<400> 30

Gly Thr Tyr Leu Tyr Asn Asp Cys Pro Gly Pro Gly Gln  
1 10

<210> 31

<211> 13

<212> PRT

<213> Artificial Sequence

<220>

<220> Description of Artificial Sequence: TNF-BP tryptic cleavage peptide

<210>

<211> UNSURE

<220> (9)..(11)

<220> Identity of "Xaa" could not be determined.

<400> 31

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1 5 10

<210> 32

<211> 20

<212> PRT

<213> Artificial Sequence

<200>

<220> Description of Artificial Sequence: TNF-BP tryptic cleavage peptide

<400> 32

Lys Glu Met Gly Gln Val Glu Ile Ser Ser Cys Thr Val Asp Arg Asp  
1 5 10 15

Thr Val Cys Gly  
20

<210> 33

<211> 19

<212> PRT

<213> Artificial Sequence

<200>

<220> Description of Artificial Sequence: TNF-BP tryptic cleavage peptide

<220>

<221> UNSURE

<222> (6)

<223> Identity of "Xaa" could not be determined.

<231>

<232> UNSURE

<233> (18)

<234> Identity of "Xaa" could not be determined.

<241>

Tyr . Ile His Pro Gln Xaa Asn Ser Ile Cys Cys Thr Lys Cys His Lys  
i 5 10 15

Xaa Tyr

<210> 34

<211> 18

<212> PRT

<213> Artificial Sequence

<214>

<215> Description of Artificial Sequence: TNF-BP trypic  
cleavage peptide

<220>

<221> UNSURE

<222> (16)..(17)

<223> Identity of "Xaa" could not be determined.

<240> 34

Gly Thr Tyr Leu Tyr Asn Asp Cys Pro Gly Pro Gly Gln Asp Thr Xaa  
i 5 10 15

Xaa Arg

<210> 35

<211> 8

<212> PRT

<213> Artificial Sequence

<214>

<215> Description of Artificial Sequence: TNF-BP trypic  
cleavage peptide

<240> 35

Leu Cys Leu Pro Gln Ile Glu Asn  
1 5

<210> 36

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: TNF-BP tryptic cleavage peptide

<220>

<221> UNSURE

<222> (?)

<223> Identity of "Xaa" could not be determined.

<400> 36

Gln Asn Thr Val Cys Thr Xaa His Ala Gly Phe Phe Ieu Arg  
1 2 3 4 5 6 7 8 9 10

<210> 37

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: TNF-BP tryptic cleavage peptide

<400> 37

Ser Ieu Glu Cys Thr Lys Leu Cys Leu Pro Gln Ile Glu Asn  
1 2 3 4 5 6 7 8 9 10

<210> 38

<211> 15

<212> PRT

<213> Homo sapiens

<220>

<223> Description of Artificial Sequence: TNF-BP tryptic cleavage peptide

<400> 38

Asp Ser Val Cys Pro Gln Gly Lys Tyr Ile His Pro Gln  
1 2 3 4 5 6 7 8 9 10

<210> 39

<211> 7

<212> PRT

<213> Homo sapiens

<220>

<223> Description of Artificial Sequence: TNF-BP tryptic cleavage peptide

<400> 39

Gln Gly Lys Tyr Ile His Pro  
1 2 3 4 5

<210> 40  
<211> 20  
<212> DNA  
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<220>  
<223> Description of Artificial Sequence: Hybridization probe  
  
<400> 40  
cagggttaat atattccatcc 16  
  
<210> 41  
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<223> Description of Artificial Sequence: Hybridization probe  
  
<400> 41  
cagggttaat acatccatcc 19  
  
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<400> 42  
caaggttaat atataccatcc 20  
  
<210> 43  
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<223> Description of Artificial Sequence: Hybridization probe  
  
<400> 43  
caaggttaat atattccatcc 20  
  
<210> 44  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>

<221> Description of Artificial Sequence: Hybridization probe

<400> 44

caatggatgt acatccaccc

20

<220> 45

<221> 20

<222> DNA

<223> Artificial Sequence

<400>

<221> Description of Artificial Sequence: Hybridization probe

<400> 45

caatggatgt atatccatcc

20

<220> 46

<221> 20

<222> DNA

<223> Artificial Sequence

<400>

<221> Description of Artificial Sequence: Hybridization probe

<400> 46

caatggatgt atattccatcc

20

<220> 47

<221> 20

<222> DNA

<223> Artificial Sequence

<400>

<221> Description of Artificial Sequence: Hybridization probe

<400> 47

caatggatgt acatccaccc

20

<220> 48

<221> 20

<222> DNA

<223> Artificial Sequence

<400>

<221> Description of Artificial Sequence: Hybridization probe

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<401> 51		
caaggaaat atatacatcc	20	
<310> 52		
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<401> 52		
Glu Cys Gly Ser Gly Ser Phe Thr Ala Ser Glu Asn Asn Lys		
1	5	10
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<210> 14

<211> PFT

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<223> Description of Artificial Sequence: TNF-BP tryptic cleavage peptide

<300> 15

Glu Cys Gly Ser Gly Ser Phe Thr Ala Ser Cys Asn Asn Lys  
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<110> 14

<111> 6

<112> PFT

<113> Artificial Sequence

<120>

<223> Description of Artificial Sequence: TNF-BP tryptic cleavage peptide

<300> 14

Phe Thr Ala Ser Glu Asn Asn Lys  
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<110> 55

<111> 8

<112> PFT

<113> Artificial Sequence

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<223> Description of Artificial Sequence: TNF-BP tryptic cleavage peptide

<400> 55

Phe Thr Ala Ser Cys Asn Asn Lys  
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<110> 56

<111> 30

<112> DNA

<113> Artificial Sequence

<120>

<223> Description of Artificial Sequence: Hybridization probe

<400> 56

caatcacgaa qactcttggtt gttcccttaggg

30

<210> 67

<211> 60

<212> DNA



<400> 61  
aaatutcggt cactcttgtt gttccctagg 30

<210> 62  
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<212> DNA  
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<214>  
<215> Description of Artificial Sequence: Hybridization probe

<400> 62  
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<210> 63  
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<212> DNA  
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<214>  
<215> Description of Artificial Sequence: Hybridization probe

<400> 63  
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<210> 64  
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<210> 65  
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<214>  
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<400> 65  
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<400> 69  
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1 5 10 15  
Cys His Lys Gly Thr Tyr Leu Tyr Asn Asp Cys Pro Gly Pro Gly Gln  
20 25 30  
Asp Thr Asp Cys Arg Glu Cys Gln Ser Gly Ser Phe Thr Ala Ser Glu  
35 40 45  
Asn Asn Lys  
50

<210> 70  
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EBI-1786

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<210> 71  
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EBI-1729

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cttccaucgt tgctggcg ttcc 25

<210> 72  
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<212> DNA  
<213> Artificial Sequence

<210>  
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EBI-1733

<400> 72  
gttccggattt gattatttgcg tag 23

<210> 73  
<211> 23  
<212> DNA





212 72  
211 81  
212 DNA  
213 Artificial sequence

220  
223 Description of Artificial Sequence: PCR primer  
EB1-2442

100 - 81  
ttatcgttgc ttatatttgc ttctgtttca ctatgtttca ctatgtttca ctatgtttca 60  
ttatgtttca ctatgtttca ctatgtttca 81

210 83  
211. 17  
212. DNA  
213. Artificial Sequence

4226  
4227 Description of Artificial Sequence: PCR primer  
EBI-1922

<400 83  
gaggtgc aa ttgaagc 17

<..110> 84  
<..111> 17  
<..112> DNA  
<..113> Artificial Sequence

<120<125 Description of Artificial Sequence: PCR primer  
EBI-2316

attcatgcggcccttag 17

<215> 85  
<211> 17  
<212> DNA  
<213> Artificial Sequence

221  
221. Description of Artificial Sequence: PCR primer  
EBI-2467

400 55  
gtcggttagca ccaagga 17

•Z10< 86  
•Z11< 17  
•Z12< DNA  
•Z13< Artificial Sequence

•Z10<  
•Z13< Description of Artificial Sequence: PCR primer  
EBI-1986

<400> 86  
gtttttcccaag tcacgac

17

•Z10< 87  
•Z11< 18  
•Z12< DNA  
•Z13< Artificial Sequence

•Z20<  
•Z23< Description of Artificial Sequence: Sequencing  
primer EBI-Z112

<400> 87  
gtccaaattat gtcacaccc

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